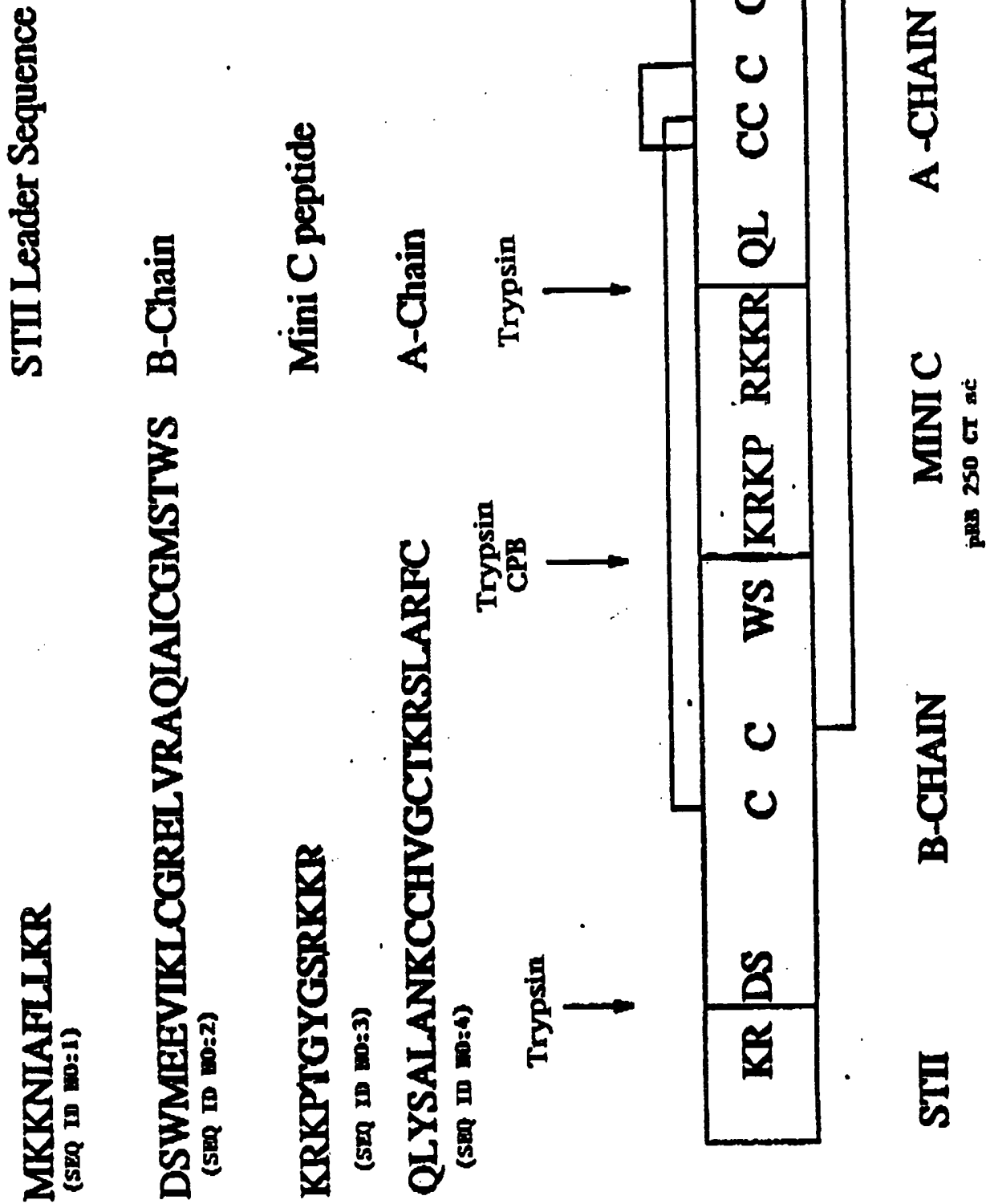


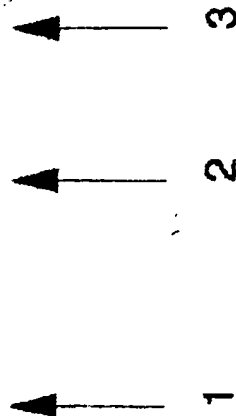
FIG. 1



Plasmid Name	Leader Sequence	C chain sequence	Cleaving Enzymes
pRB250CT ^{sc}	MIKKNIAFLKR	KRIKPTGYGSRARRK 5	Trypsin and carboxy-peptidase C (CPB)
pREL CIII	MIKKNIAFLKR	DKKRTGYGSRARRK 6	AspN and LysC
pREL CaspN	MIKKNIAFLKR	DKKRTGYGSRARRK 7	aspN and trypsin or ArgC
pREL LysC	MIKKNIAFLKR	KRIKPTGYGSRARRK 8	LysC and CPB

FIG. 2

STII	B-CHAIN	MINI-C	A-CHAIN
------	---------	--------	---------

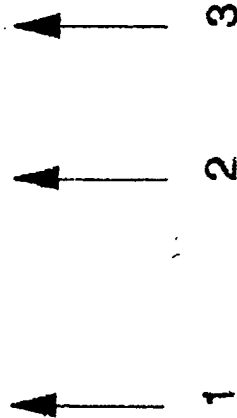


CONST	STII/B-CHAIN	BC/MC	MC/AC	SITE	ENZYMES
pRB250CTsc	↓ 1 KR DS	↓ 2 ...WS KRKP...RKRR QL	↓ 3	1	TRYP.; ASP-N
				2	TRYP.; ARG-C; LYS-C; ALL WITH CPB
				3	TRYP.; ARG-C

MOST FAVORABLE COMBINATIONS

ARG-C / CPB
TRYPSIN / CPB

FIG. 2A

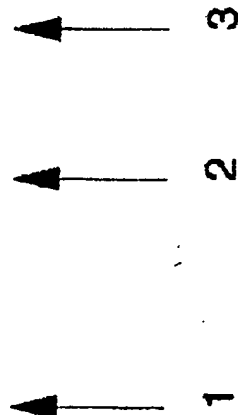


CONST	STII/B-CHAIN	BC / MC	MC / AC	SITE	ENZYMES
pRELCIII	↓ 1	↓ 2	↓ 3	1	TRYP.; ASP-N
	KR DS	...WS DKKR	...RRRK Q	2	ASP-N
				3	TRYP.; LYS-C

MOST FAVORABLE COMBINATIONS

ASP-N / LYS-C
ASP-N / TRYPSIN

FIG. 2B



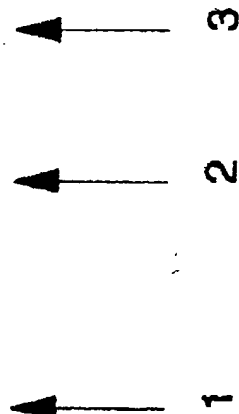
CONST	STII/B-CHAIN	BC / MC	MC / AC	SITE	ENZYMES
pRELCLysC	↓ 1 KR DS	↓ 2 WS KRK	↓ 3 ...RRRK Q	1	TRYP.; ASP-N
				2	TRYP.; ARG-C LYS-C; ALL WITH CPB
				3	TRYP.; LYS-C

MOST FAVORABLE COMBINATIONS

TRYPSIN / CPB
 TRYPSIN / LYS-C / CPB
 ARG-C / LYS-C / CPB

FIG. 2C

STII	B-CHAIN	MINI-C	A-CHAIN
------	---------	--------	---------



CONST	STII/B-CHAIN	BC / MC	MC / AC	SITE	ENZYMES
pRELCaspN	↓ 1 KR DS	↓ 2 ...WS DKKR	↓ 3 ...RKKR Q	1 2 3	TRYP.; ASP-N ASP-N TRYP.; ARG-C

MOST FAVORABLE COMBINATIONS

ASP-N / ARG-C
ASP-N / TRYPSIN

FIG. 2D

ATG AAA AAG AAT ATC GCA TTT CTT CTT AAA GGG GAC TCA 36
 Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser
 1 5 10
STII leader + KR

TGG ATG GAG GAA GTT ATT AAA TTA TGC GGC CGC GAA TTA 75
 Trp Met Glu Glu Val Ile Lys Leu Cys Gly Arg Glu Leu
 15 20 25
B-chain relaxin

GTT CGC GCG CAG ATT GCC ATT TGC GGC ATG AGC ACC TCG 114
 Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp
 30 35

AGC AAA AGG AAA CCC ACT GGT TAT GGT TCT CGA AAA AAG 153
 Ser Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys
 40 45 50
Synthetic DNA Encoding C-Peptide

AGA CAA CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC CAT 192
 Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His
 55 60
A-chain relaxin

GTT GGT TGT ACC AAA AGA TCT CTT GCT AGA TTT TGC 228
 Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys
 65 70 75 76

FIG. 3

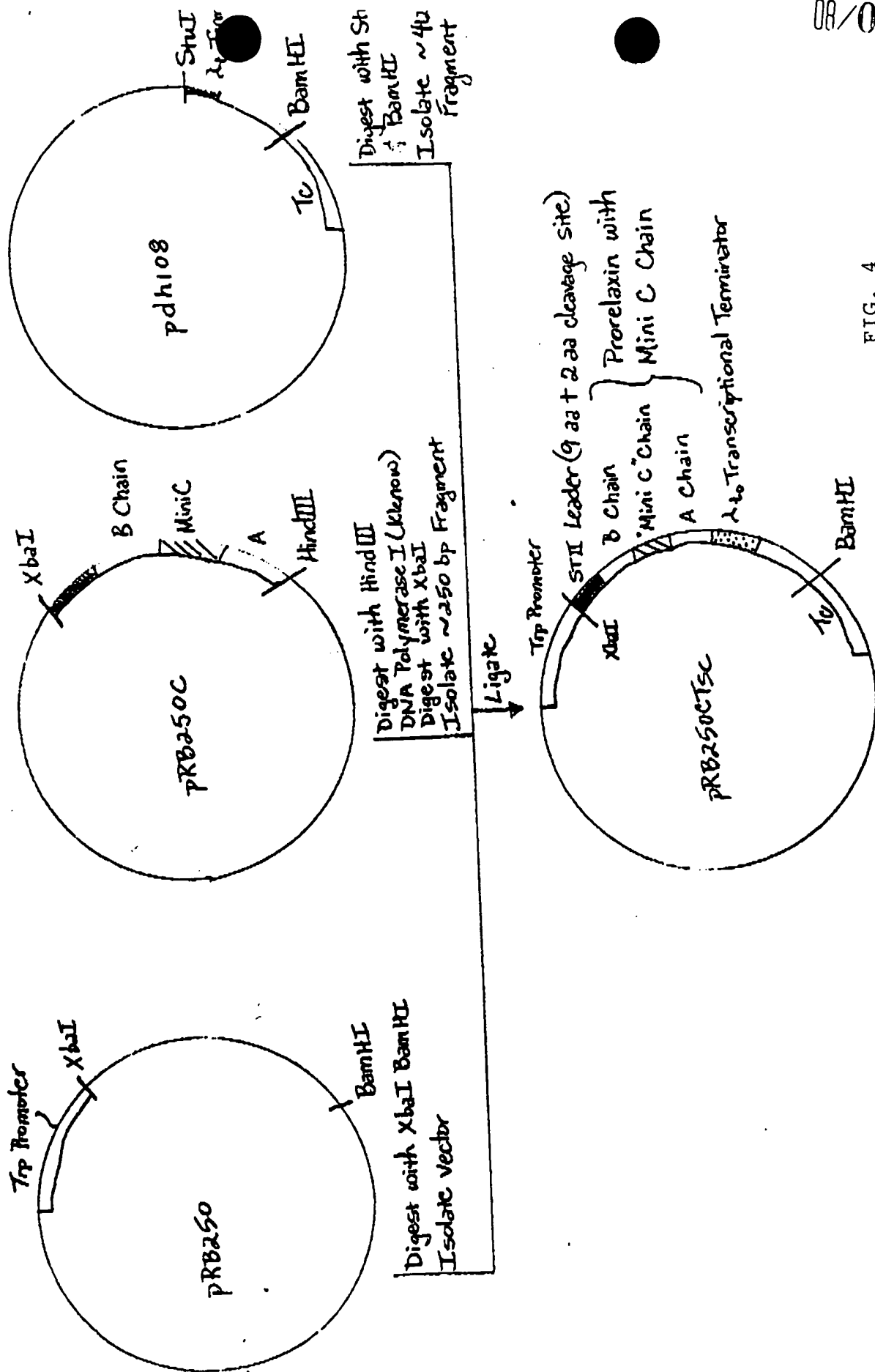


FIG. 4

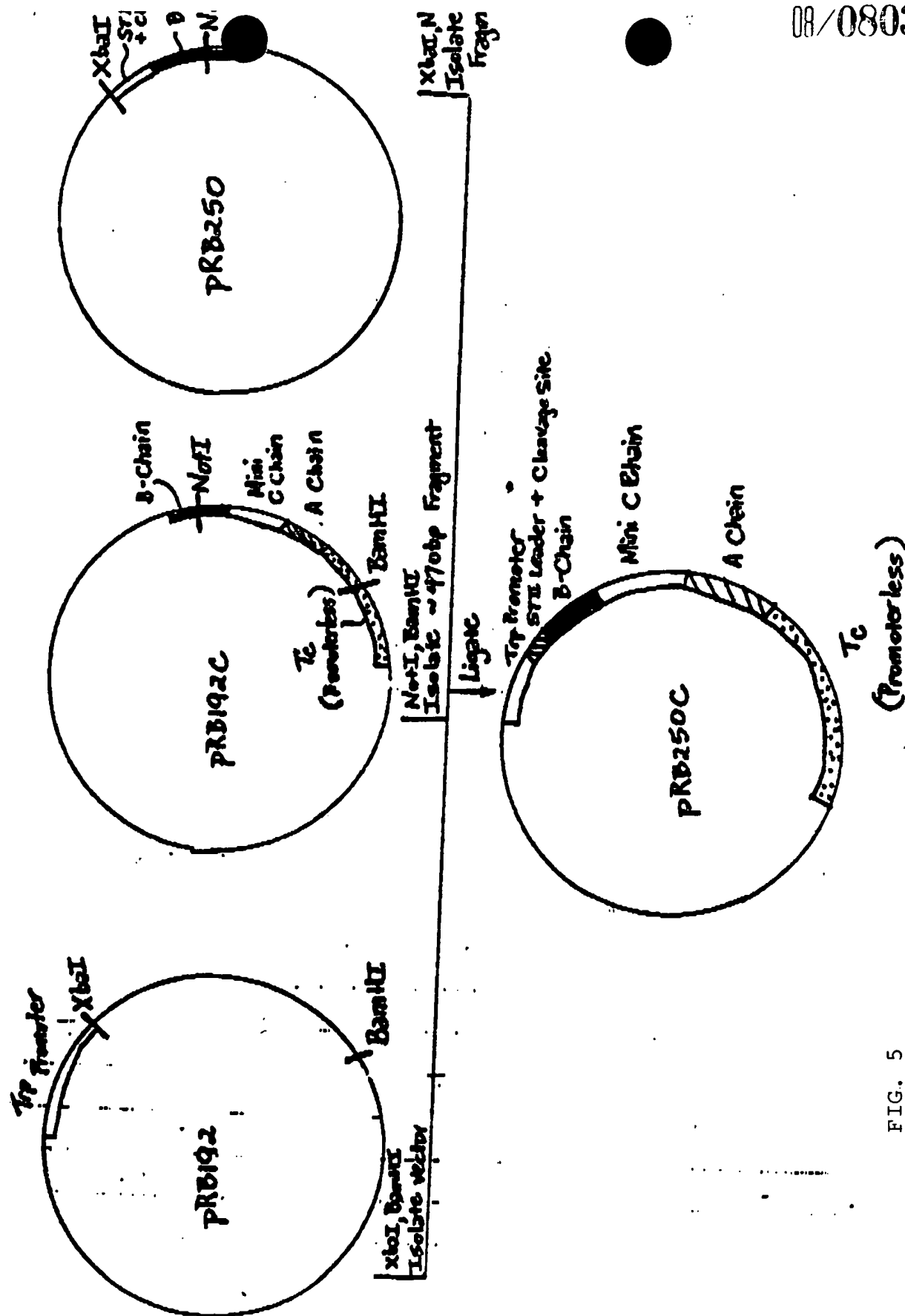


FIG. 5

FIG. 6

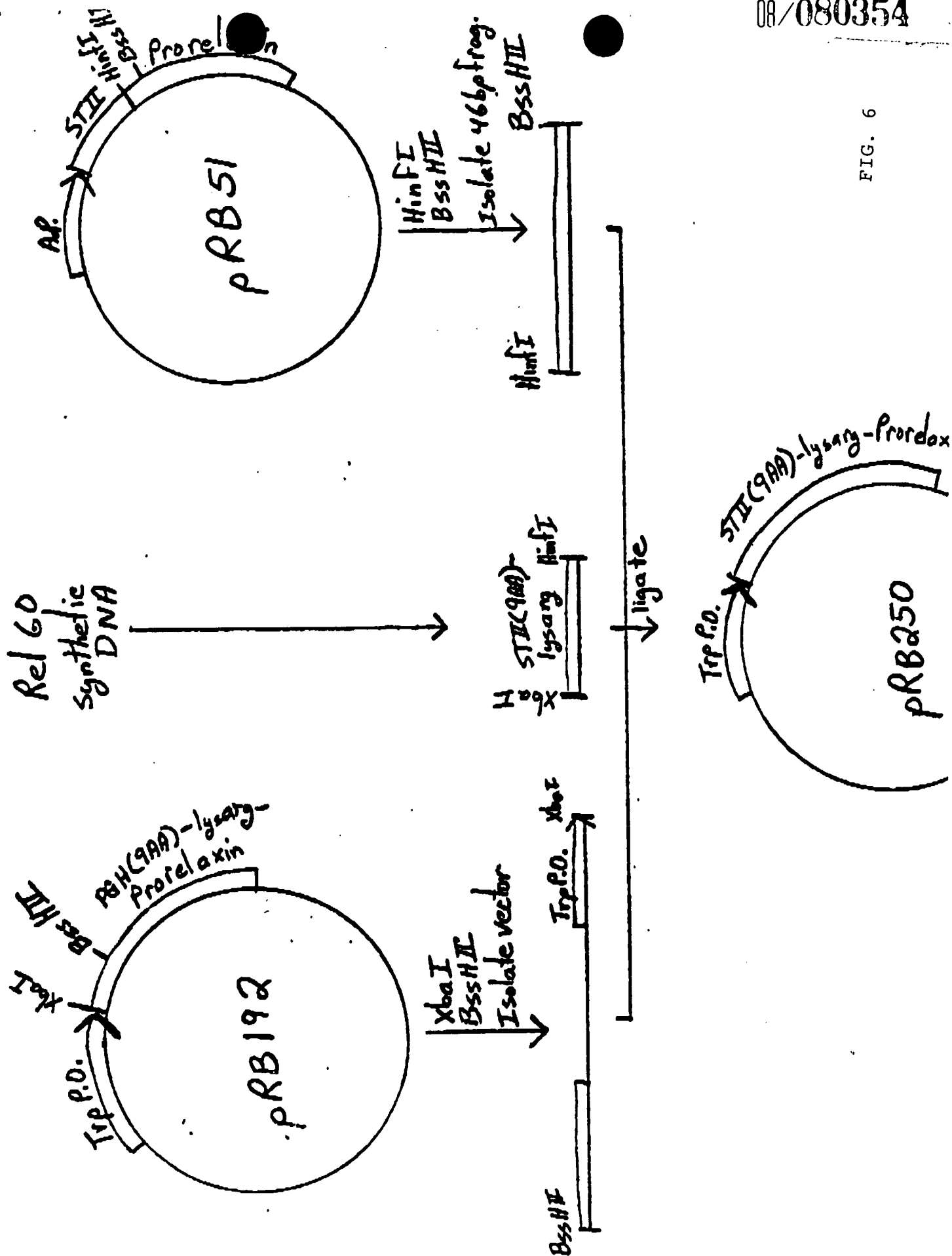
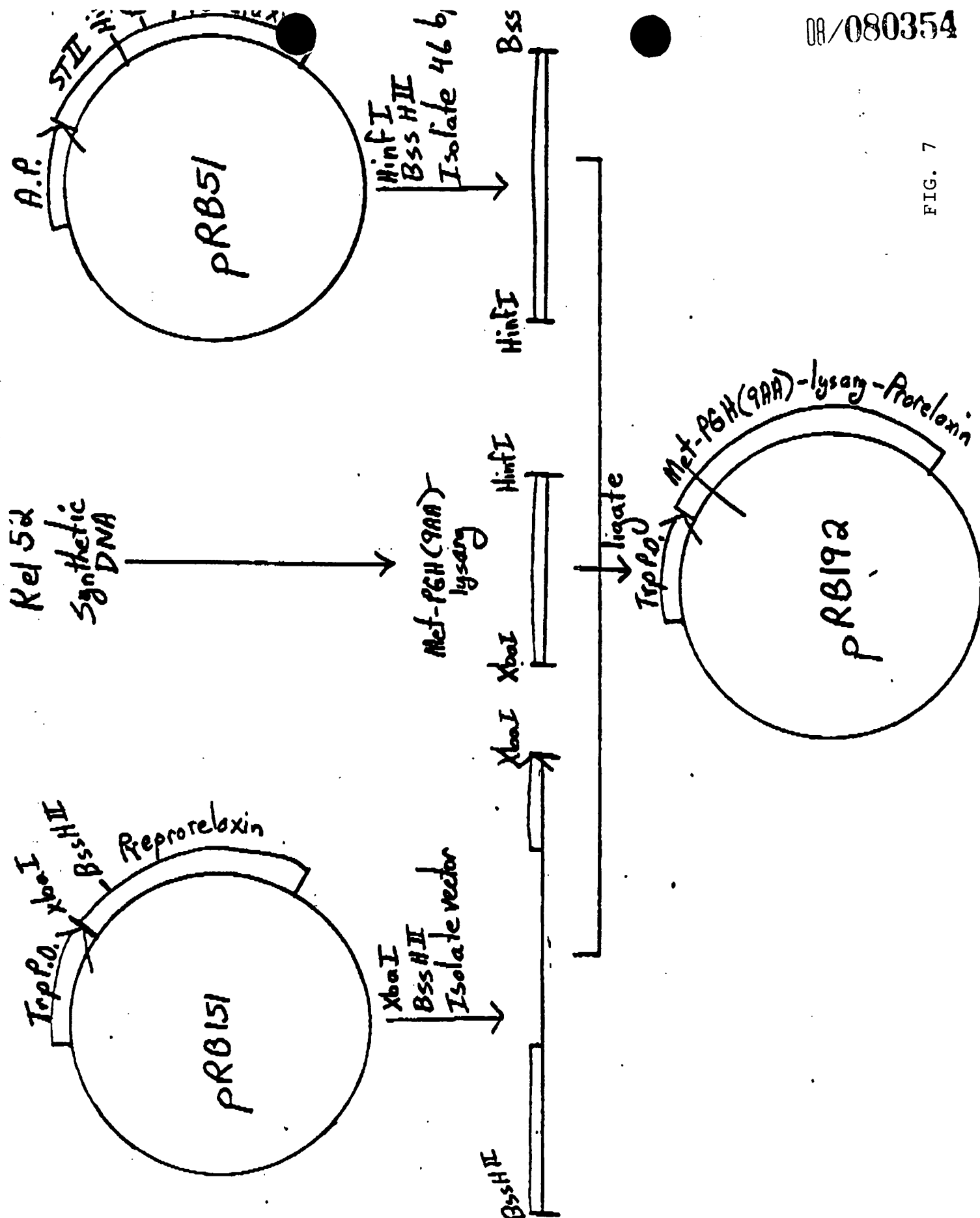


FIG. 7



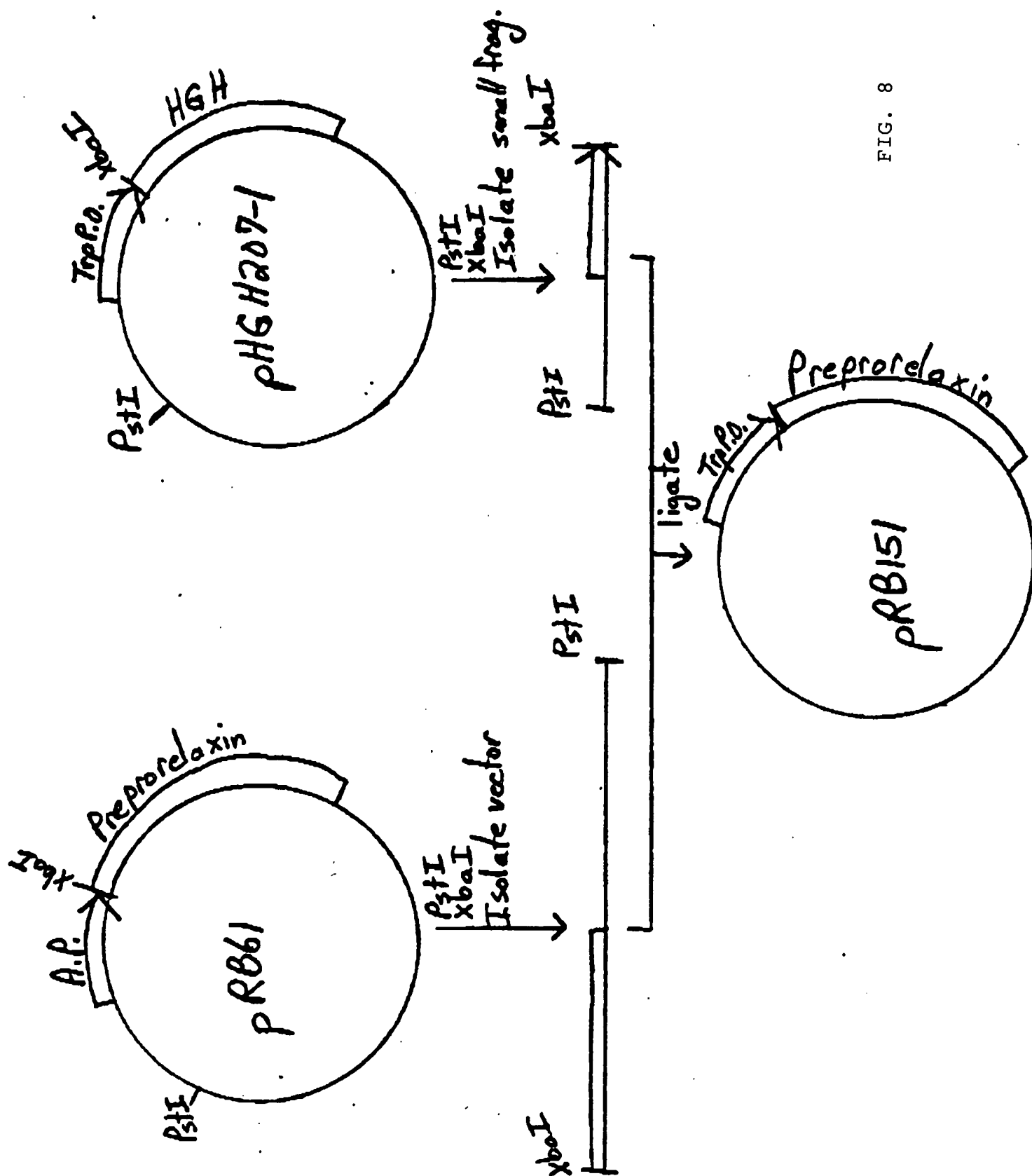


FIG. 8

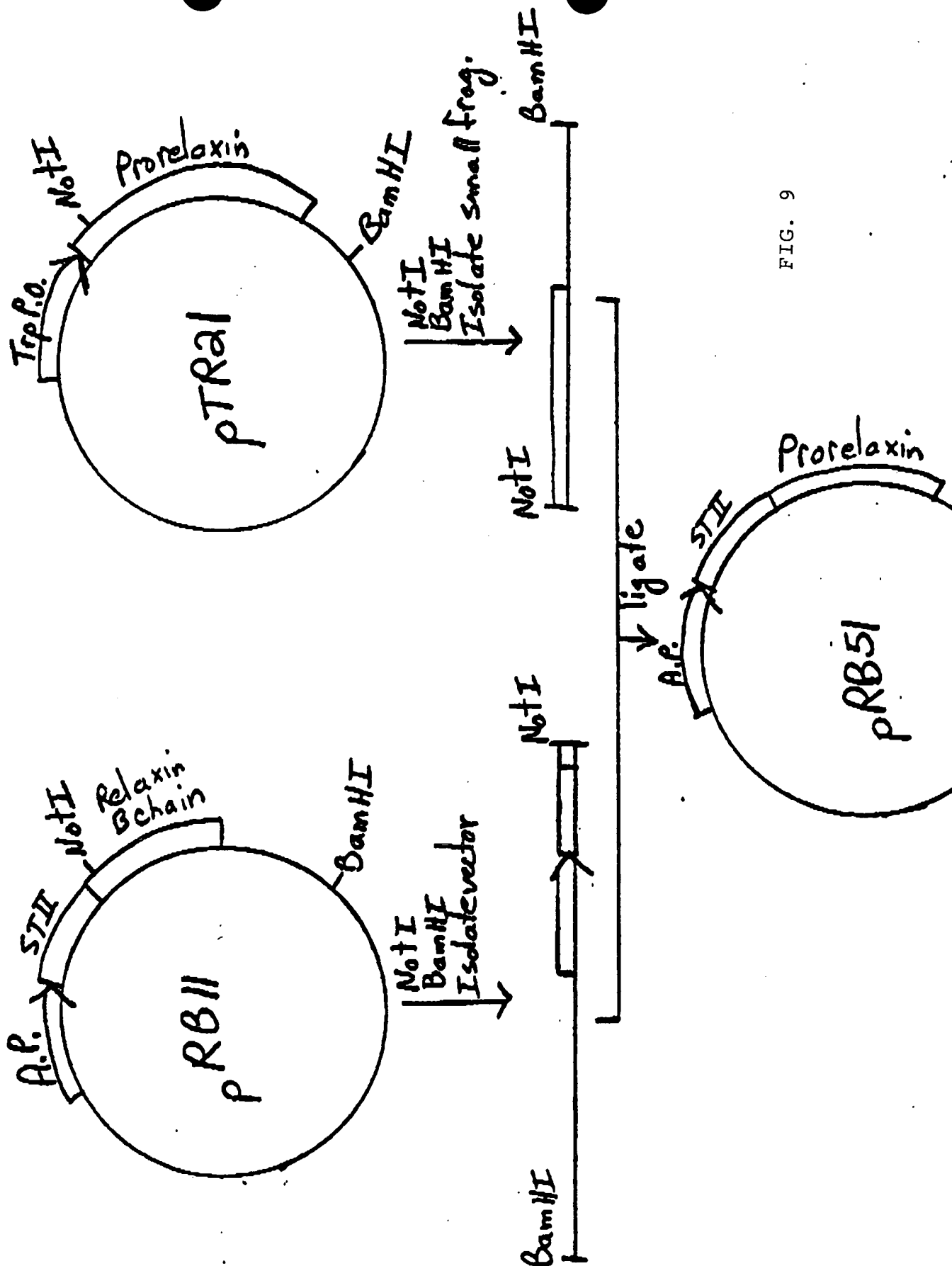


FIG. 9

GlyArgGluLeuValArgAlaGlnIleAlaIleCysGlyMetSerThrTrpSerLysArgSerLeuSerGlnGluAsp
 GCGGCCGCGAATTAGTTTCGCGCGCAGATTGCCATTTGCGGCATGAGCACCTGGAGCAAAAGGTCTCTGAGCCAGGAAGAT

 AlaProGlnThrProArgProValAlaGluIleValProSerPheIleAsnLysAspThrGluThrIleAsnMetMetSer
 GCTCCTCAGACACCTAGACCAGTGGCAGAAATTGTGCCATCCTTCATCAACAAAGATACAGAAACCATAAATATGATGTC

 GluPheValAlaAsnLeuProGlnGluLeuLysLeuThrLeuSerGluMetGlnProAlaLeuProGlnLeuGlnGlnHis
 AGAATTTGTTGCTAATTTGCCACAGGAGCTGAAGTTAACCCTGTCTGAGATGCAGCCAGCATTACCACAGCTACAACAAC

 ValProValLeuLysAspSerSerLeuLeuPheGluGluPheLysLysLeuIleArgAsnArgGlnSerGluAlaAla
 ATGTACCTGTATTAAAGATTCCAGTCTTCTCTTTGAAGAATTTAAGAACTTATTGCAATAGACAAAGTGAAGCCGCA

 AspSerSerProSerGluLeuLysTyrLeuGlyLeuAspThrHisSerArgLysLysArgGlnLeuTyrSerAlaLeuAla
 GACAGCAGTCCTTCAGAATTAAATACTTAGGCTTGGATACTCATCTCGAAAAAAGAGACAACCTCTACAGTGCATTGGC

 AsnLysCysCysHisValGlyCysThrLysArgSerLeuAlaArgPheCys
 TAATAAATGTTGCCATGTTGGTTGTACCAAAAGATCTCTTGCTAGATTTTGCTGAGATGAAGCTAATTGTGCACATCTCG

 TATAATATTCACACATATTCTTAATGACATTTCACTGATGCTTCTATCAGGTCAATTCTCATGTTTGACAGCTTATCATC

 GATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGGCACCGTGTATGAAATCTAACAATGCGCT

 CATCGTCATCTCGGCACCGTCACCCTGGATGCTGTAGGCATAGGCTTGGTTATGCCGGTACTGCCGGGCTCTTGCGGG

 ATATCGTCCATTCCGACAGCATCGCCAGTCACTATGGCGTGCTGCTAGCGCTATATGCGTTGATGCAATTTCTATGCGCA

 CCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCGCCAGTCCTGCTCGCTTCGCTACTTGGAGCCACTATCGACTA

 CGCGATCATGGCGACCACACCCGTCCTGTGGATCC

FIG. 9A

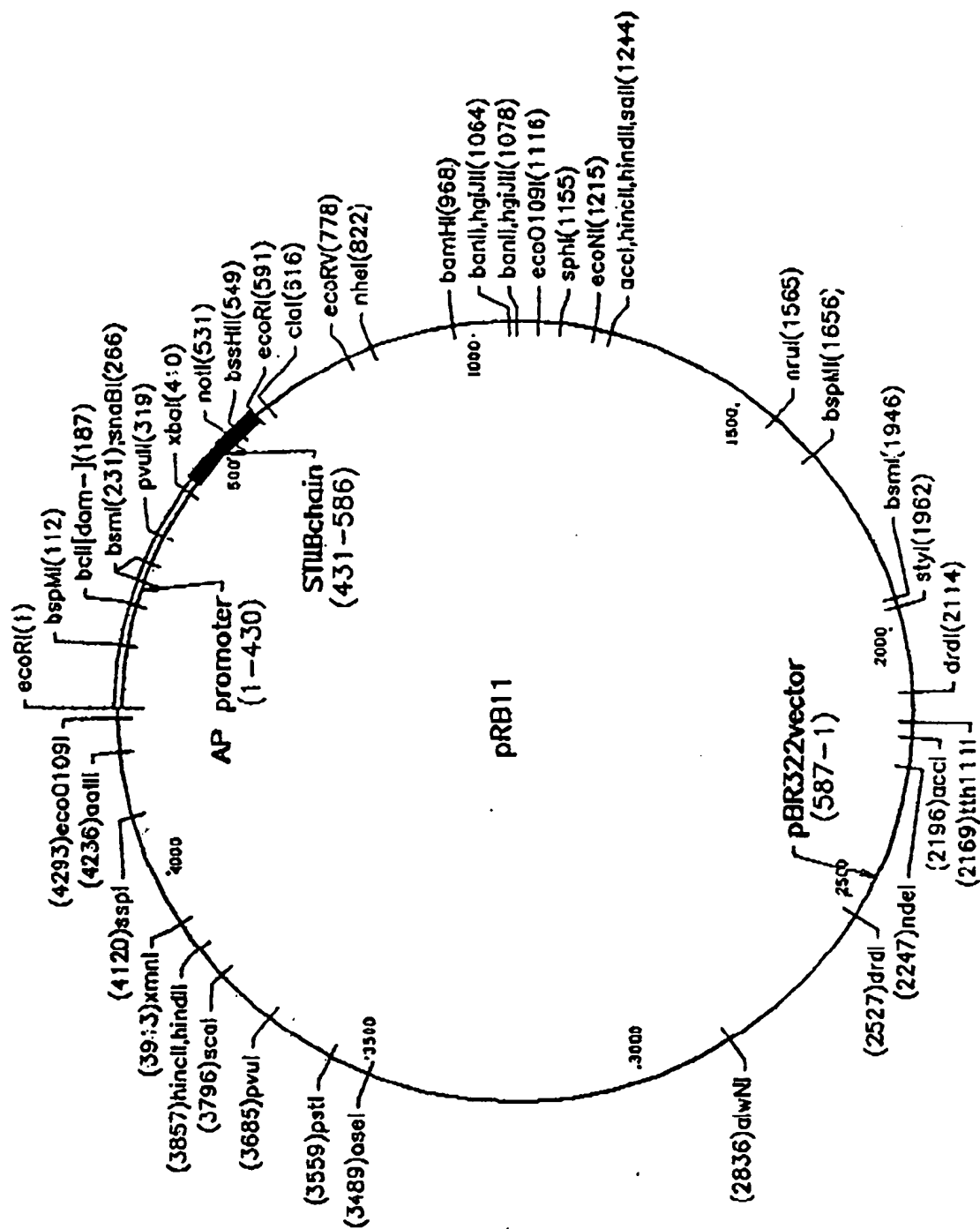
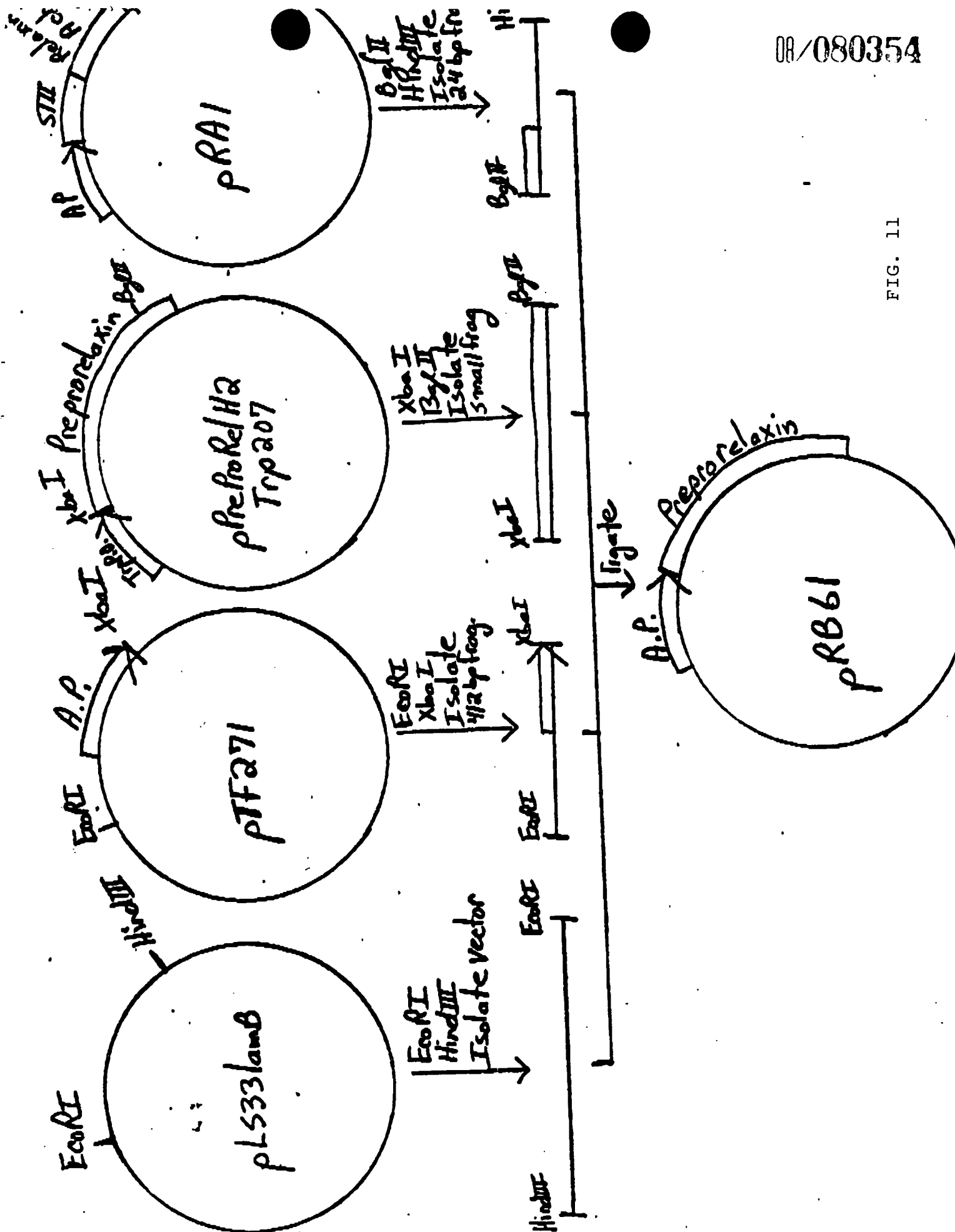


FIG. 10A

FIG. 11



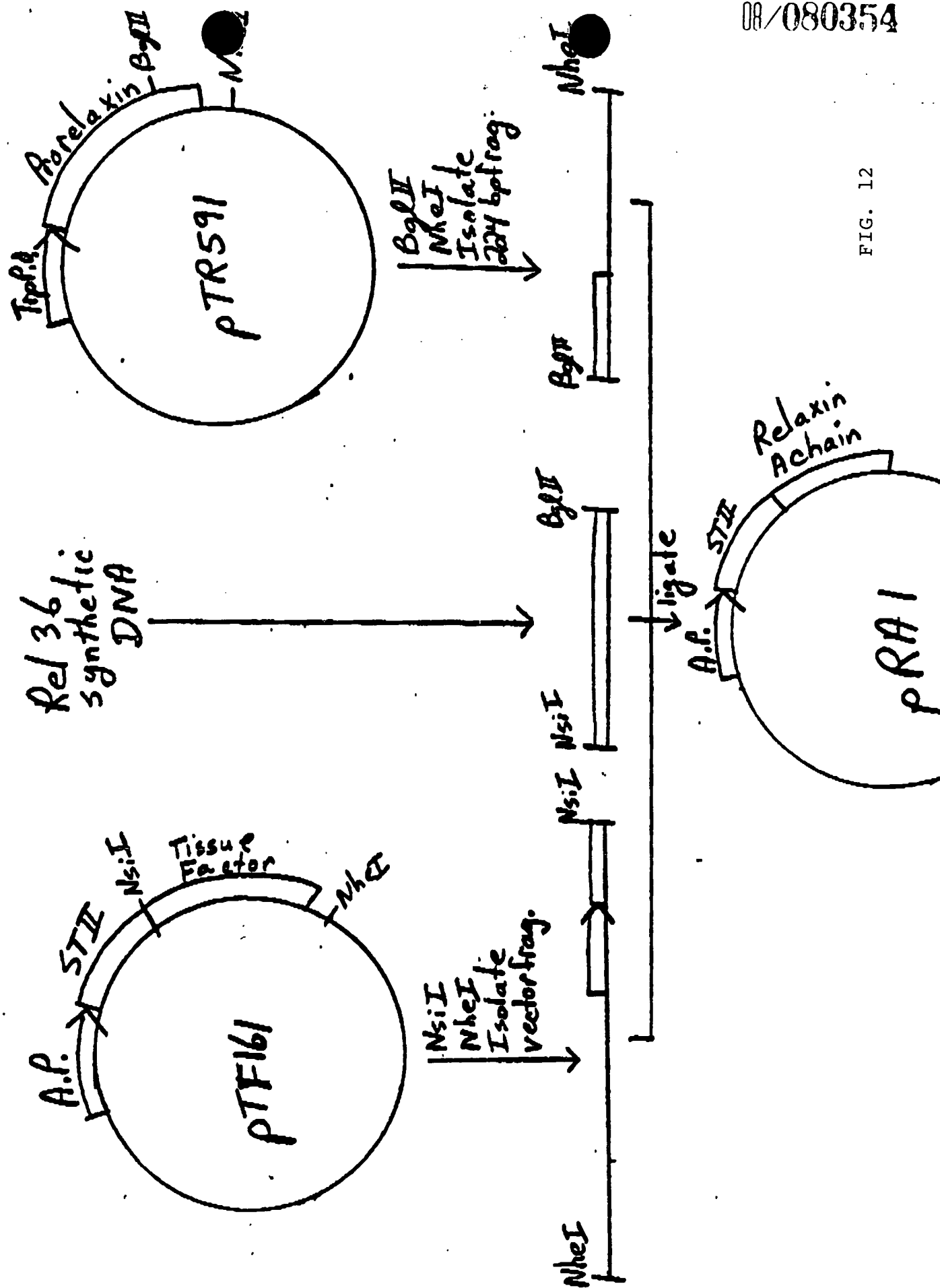


FIG. 12

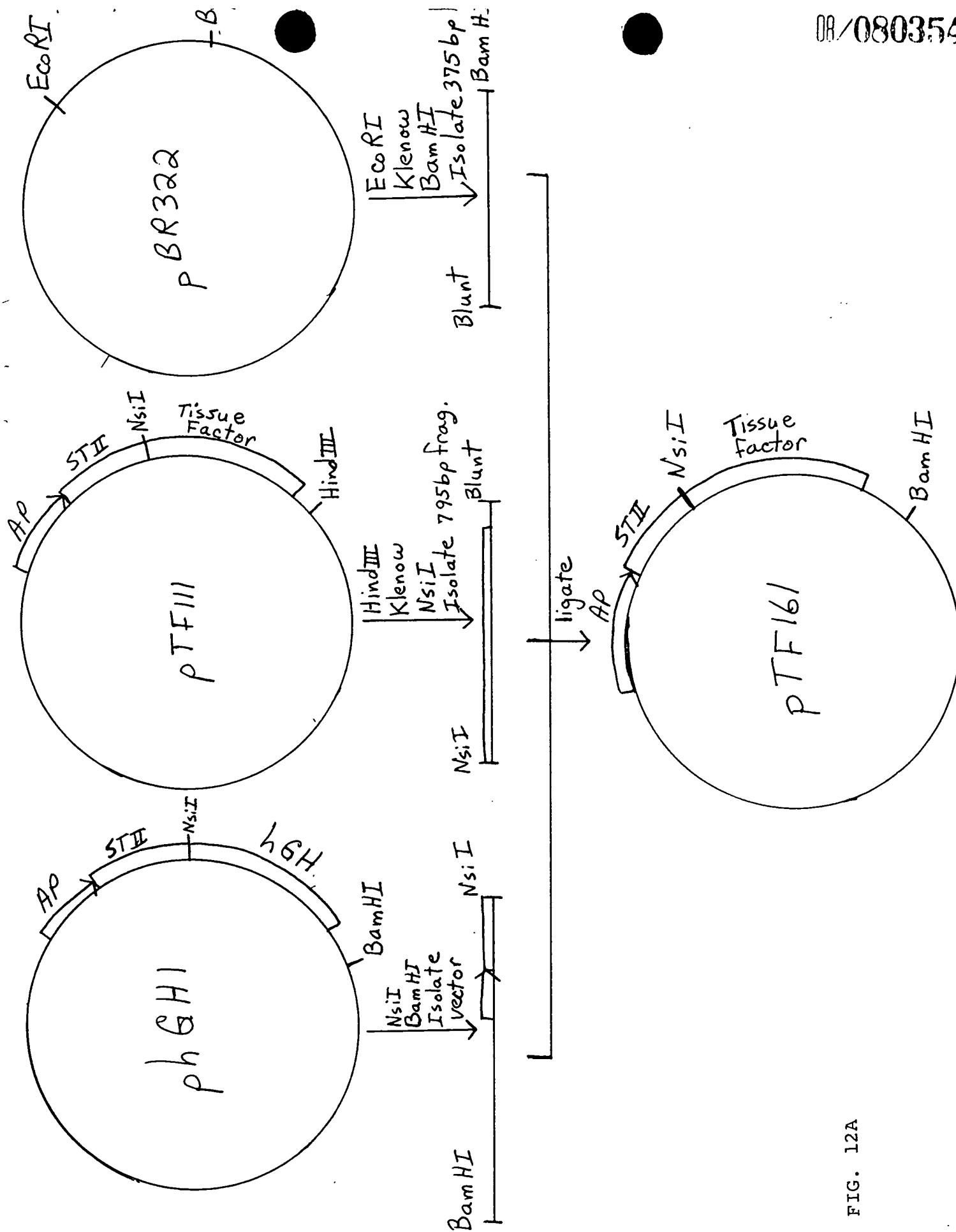
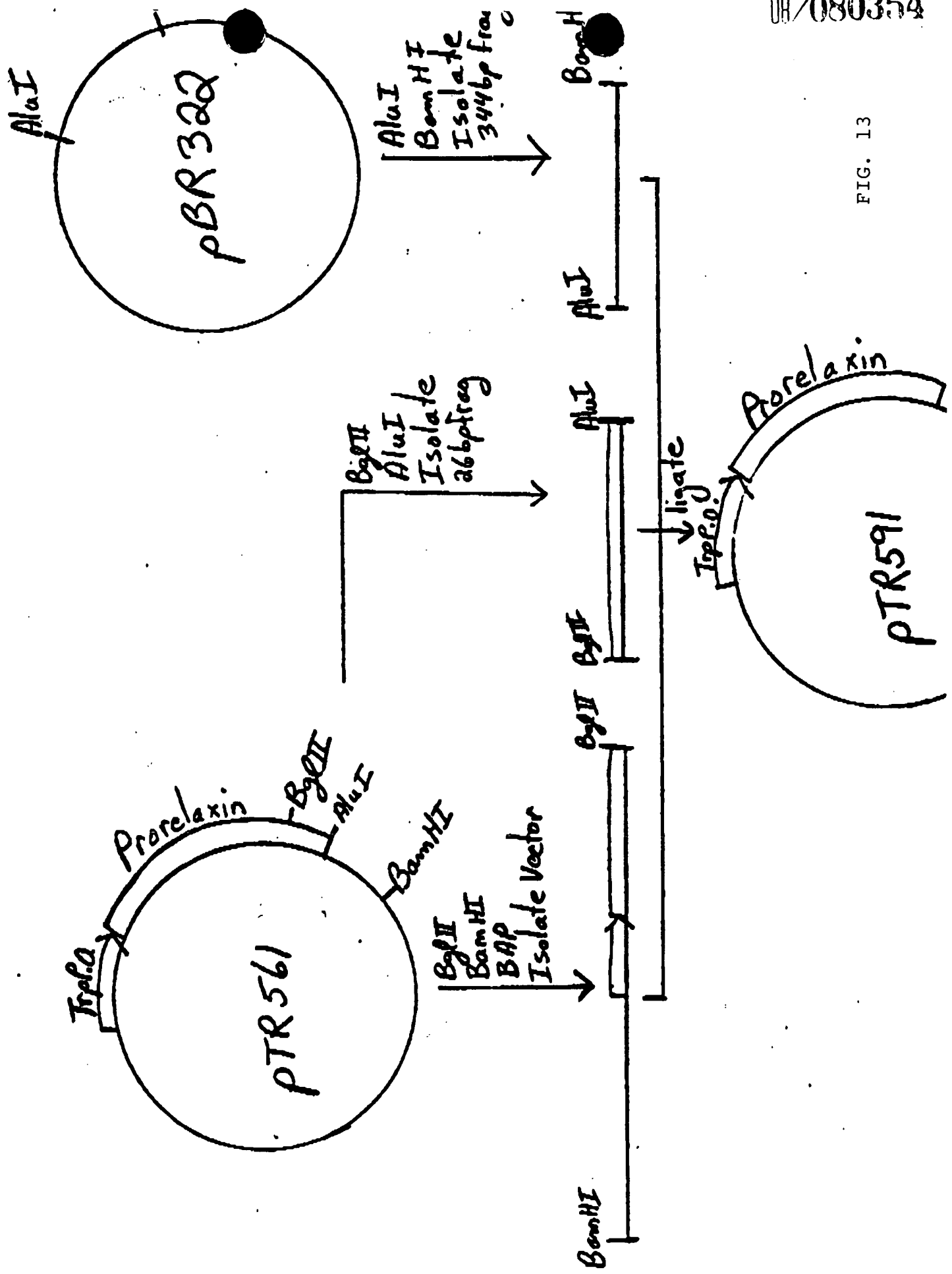
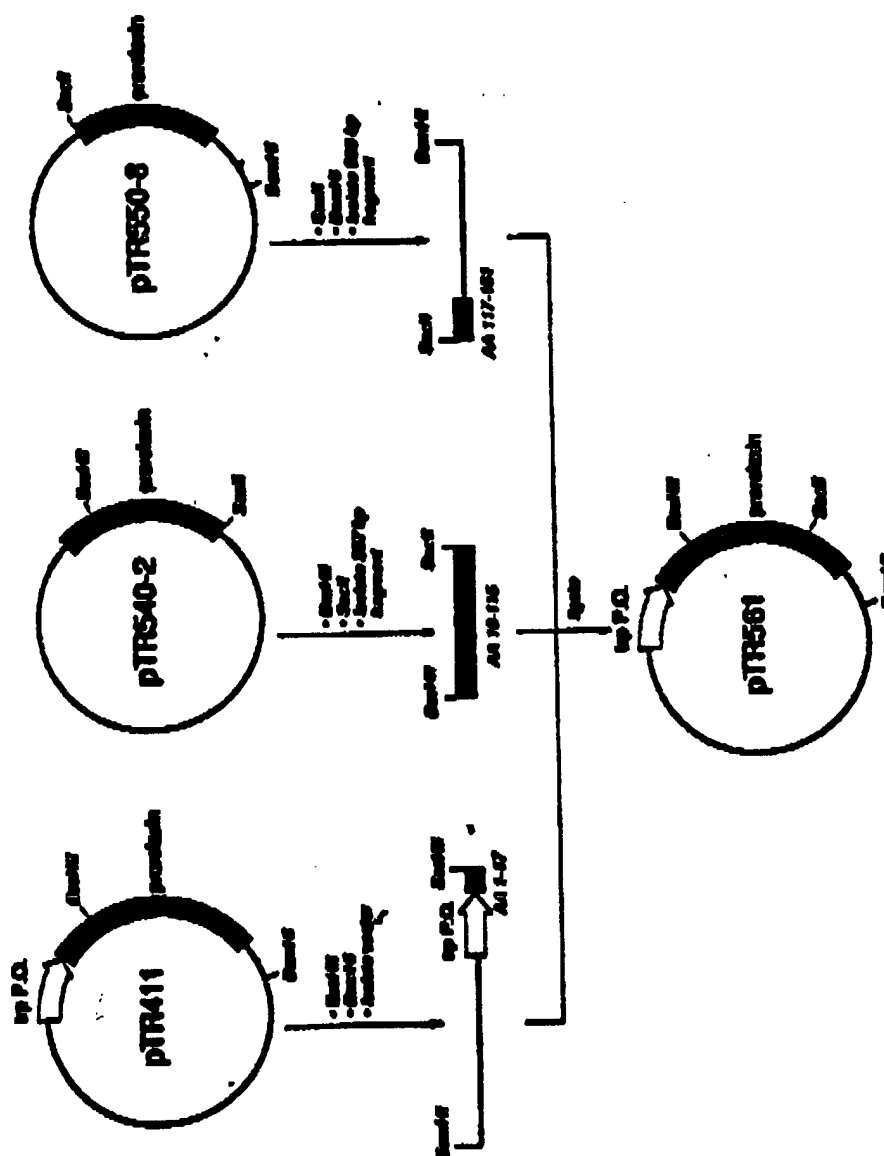


FIG. 12A

FIG. 13





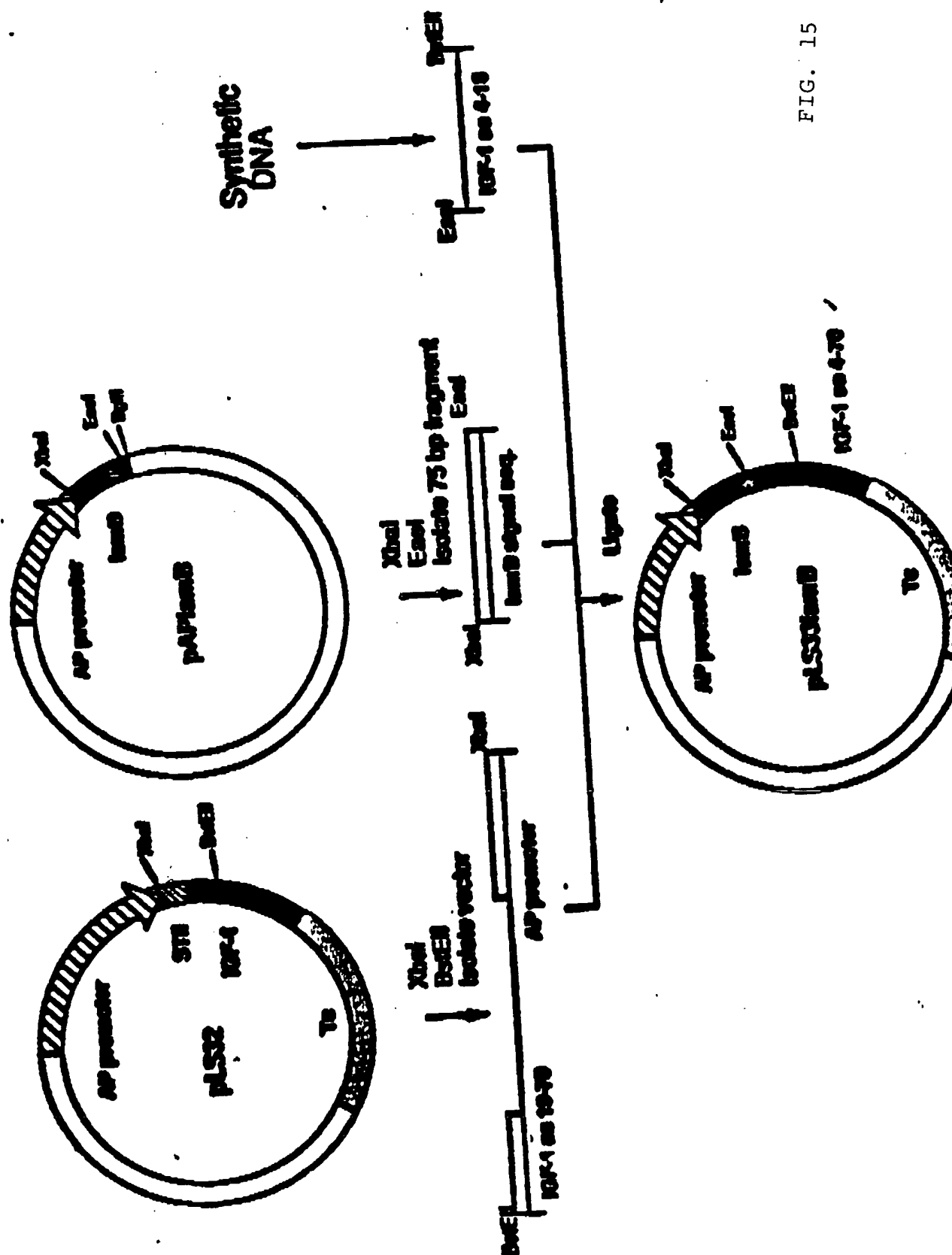


FIG. 15

GAATTCAACTTCTCCATACTTTGGATAAGGAAATACAGACATGAAAAATCTCATTGCTGAGTTGTTATTTAAGCTTGCCC
 AAAAAAGAAGAAGAGTCGAAAGAAGTGTGTGCGCAGGTAGAAGCTTTGGAGATTATCGTCACTGCAATGCTTCGCAATATG
 GCGCAAAATGACCAACAGCGGTTGATTGATCAGGTAGAGGGGGCGCTGTACGAGGTAAAGCCCGATGCCAGCATTCTCTGA
 CGACGATACGGAGCTGCTGCGCGATTACGTAAAGAAGTTATTGAAGCATCCTCGTCAGTAAAAAGTTAATCTTTTCAACA
 GCTGTCATAAAGTTGTCACGGCCGAGACTTATAGTCGCTTTGTTTTTATTTTAAATGTATTGTAACTAGTACGCAAGT

hp S.D. STII S.D. -23 -20
 TCACGTAAAAAGGGTATCTAGAGGTTGAGGTGATTTT Met Lys Lys Asn Ile Ala Phe Leu Leu Ala
 ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA

-10 1
 Ser Met Phe Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Ser Gly Thr Thr Asn Thr Val
 TCT ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TCA GGC ACT ACA AAT ACT GTG

10 20
 Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro
 GCA GCA TAT AAT TTA ACT TGG AAA TCA ACT AAT TTC AAG ACA ATT TTG GAG TGG GAA CCC

30 40
 Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser
 AAA CCC GTC AAT CAA GTC TAC ACT GTT CAA ATA AGC ACT AAG TCA GGA GAT TGG AAA AGC

50 60
 Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val
 AAA TGC TTT TAC ACA ACA GAC ACA GAG TGT GAC CTC ACC GAC GAG ATT GTG AAG GAT GTG

70 80
 Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly
 AAG CAG ACG TAC TTG GCA CGG GTC TTC TCC TAC CCG GCA GGG AAT GTG GAG AGC ACC GGT

90 100
 Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn
 TCT GCT GGG GAG CCT CTG TAT GAG AAC TCC CCA GAG TTC ACA CCT TAC CTG GAG ACA AAC

110 120
 Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val
 CTC GGA CAG CCA ACA ATT CAG AGT TTT GAA CAG GTG GGA ACA AAA GTG AAT GTG ACC GTA

130 140
 Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe
 GAA GAT GAA CGG ACT TTA GTC AGA AGG AAC AAC ACT TTC CTA AGC CTC CGG GAT GTT TTT

150 160
 Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr
 GGC AAG GAC TTA ATT TAT ACA CTT TAT TAT TGG AAA TCT TCA AGT TCA GGA AAG AAA ACA

170 180
 Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe
 GCC AAA ACA AAC ACT AAT GAG TTT TTG ATT GAT GTG GAT AAA GGA GAA AAC TAC TGT TTC

190 200
 Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val
 AGT GTT CAA GCA GTC ATT CCC TCC CGA ACA GTT AAC CGG AAG AGT ACA GAC AGC CCG GTA

210 220
 Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile Gly Ala Val
 GAG TGT ATG GGC CAG GAG AAA GGG GAA TTC AGA GAA ATA TTC TAC ATC ATT GGA GCT GTG

230 240
 Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile Ser Leu His OC*
 GTA TTT GTG GTC ATC ATC CTT GTC ATC ATC CTG GCT ATA TCT CTA CAC TAA AATTCTCATGT

TTGACAGCTTATCATCGATAAGCTTTAATGCCGTAGTTTATCAGTTAAATTGCTAACGCAGTCAGGCACCGTGTATGA
 AATCTAACAATGCCGTCATCGTCATCCTCGGCCACCGTCACCGTGGATGCTGTAGGCATAGGCTTGGTTATGCCGCTACTG
 CCGGGCCTCTTGGGGATATCGTCCATTCCGACAGCATCGCCAGTCAGTATGGCGTGTCTAGCGCTATATGCGTTGAT
 GCAATTTCTAT

FIG. 16

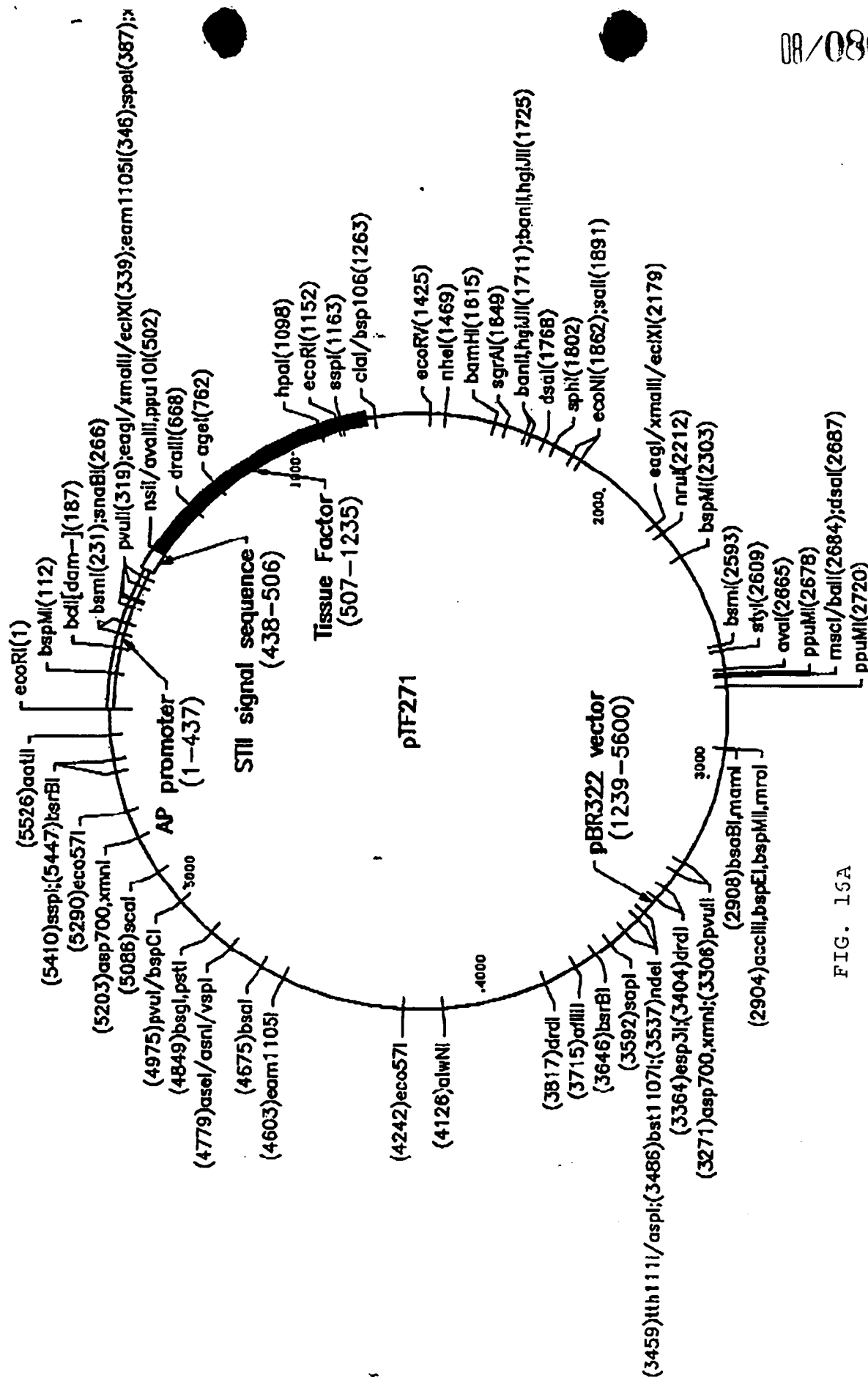


FIG. 15A

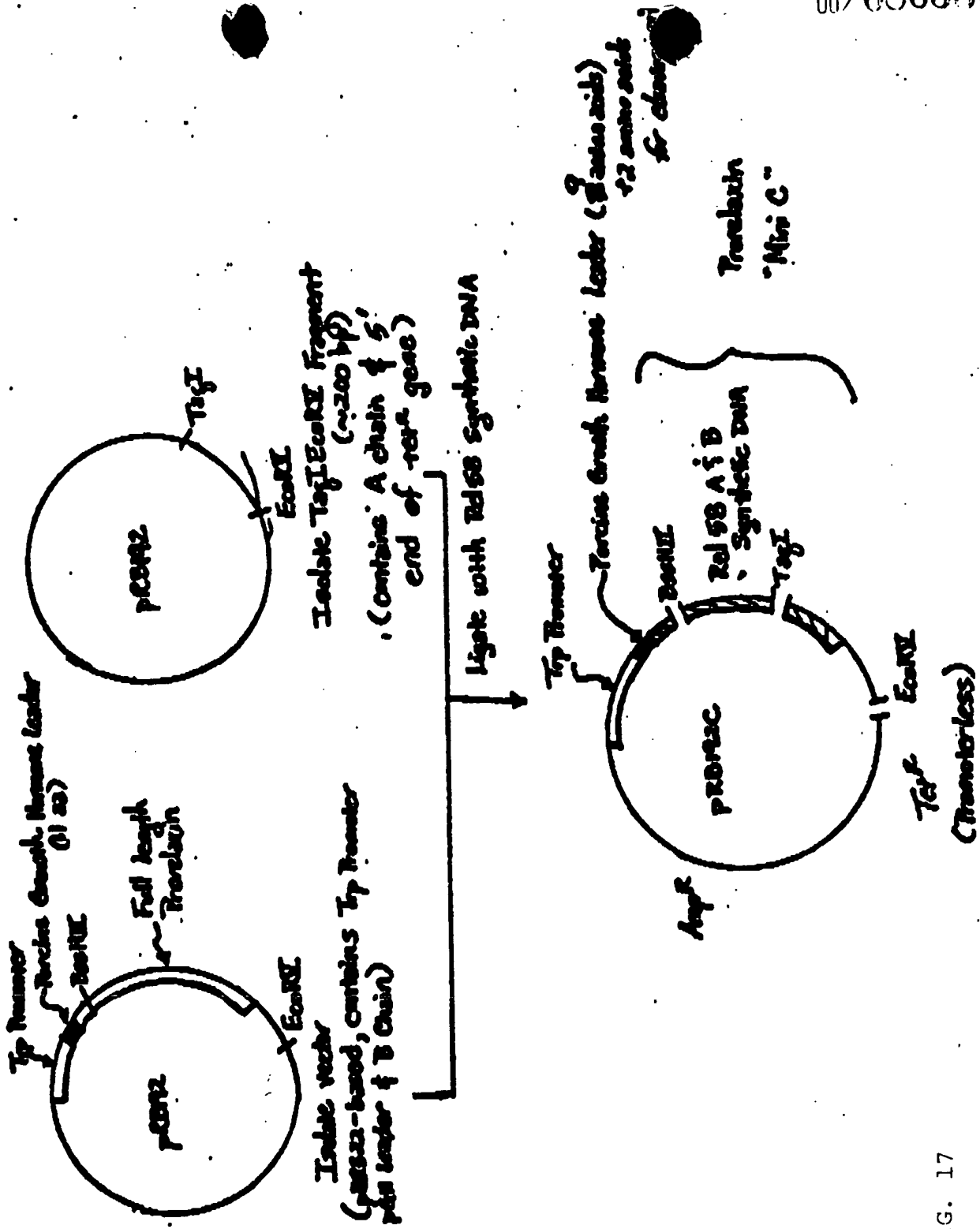
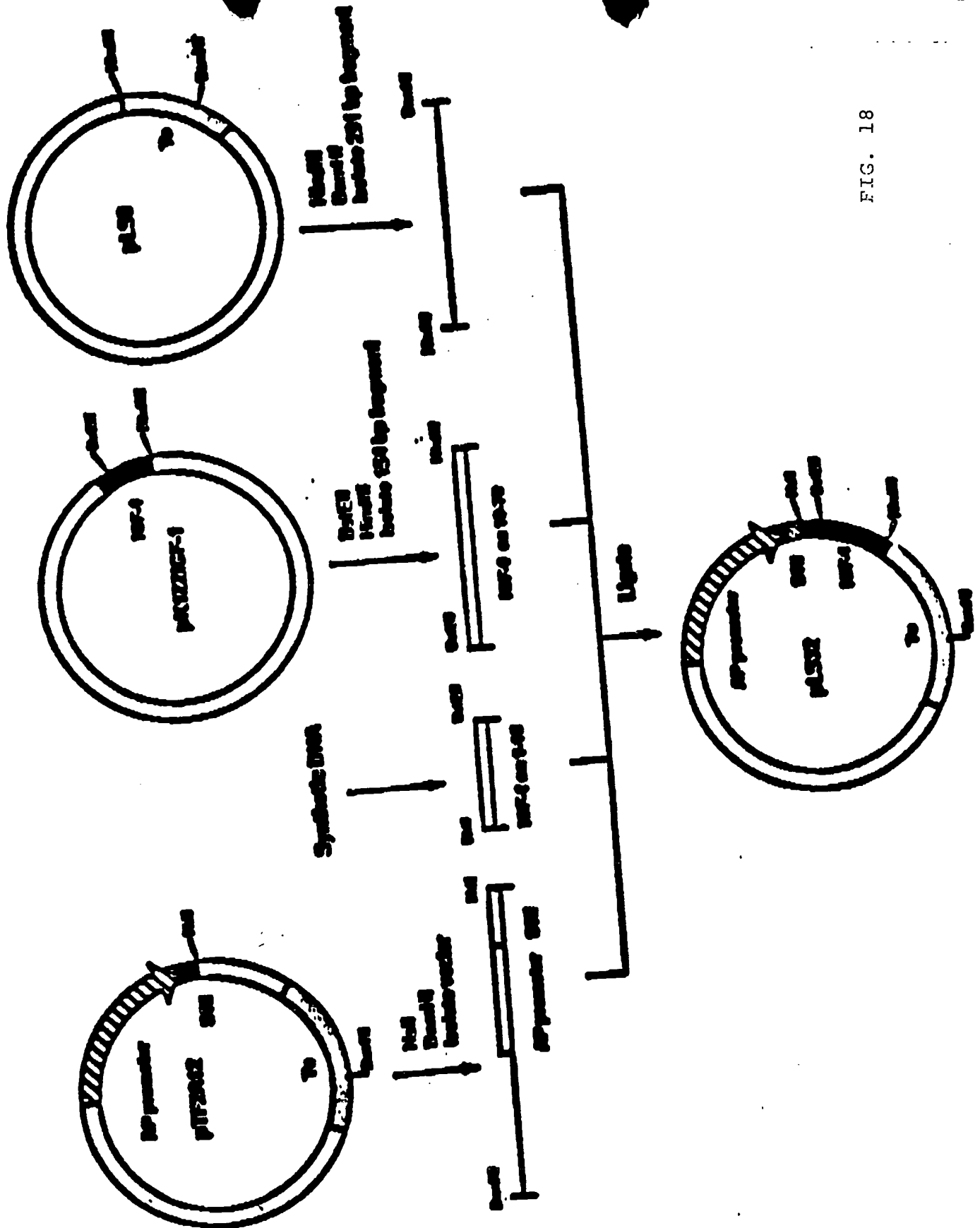


FIG. 17

FIG. 18



MetLysSerAsnAsnAlaLeuIleValIleLeuGlyThrValThrLeuAspAlaValGlyIleGlyLeuValMet
AAGCTTATGAAATCTAACAAATGCGCTCATCGTCATCCTCGGCACCGTCACCCCTGGATGCTGTAGGCATAGGCTTGGTTAT

ProValLeuProGlyLeuLeuArgAspIleValHisSerAspSerIleAlaSerHisTyrGlyValLeuLeuAlaLeuTyr
GCCGGTACTGCCGGGCCCTCTTGCGGGATATCGTCCATTCOGACAGCATCGCCAGTCACTATGGCGTGTGCTAGCGCTAT

AlaLeuMetGlnPheLeuCysAlaProValLeuGlyAlaLeuSerAspArgPheGlyArgArgProValLeuAla
ATGCGTTGATGCAATTCTATGCGCACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCGCCAGTCCTGCTCGCT

SerLeuLeuGlyAlaThrIleAspTyrAlaIleMetAlaThrThrProValLeuTrp
TCGCTACTTGGAGCCACTATCGACTACGCGATCATGGCGACCACACCCCGTCTCTGTGGATCC

FIG. 18A

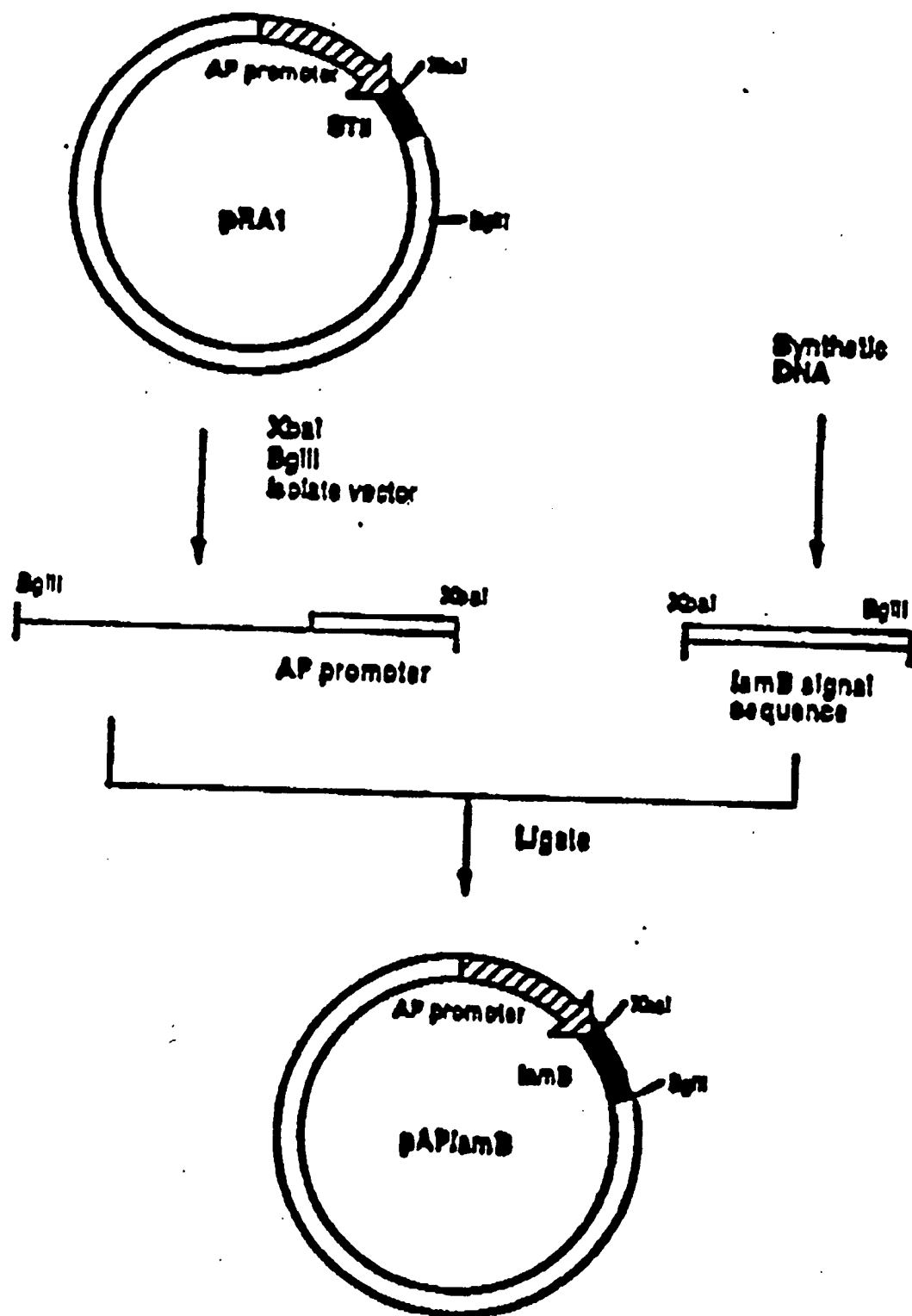


FIG. 19